

Gencore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.					
OM protein - protein search, using sw model					
Run on: January 7, 2002, 16:05:25 ; Search time 77.01 Seconds (without alignments) 22.618 Million cell updates/sec					
Title: US-08-569-749-9	perfect score: 293	sequence: .I PEQLASAGYYVGRNDVKC.....CWESGDDPWEHAKWPRCE	scoring table: BLOSUM2	GAPOP 10.0 , gapext 0.5	
Total number of hits satisfying chosen parameters: 100059	Minimum DB seq length: 0	Maximum DB seq length: 200000000	Post-processing: Minimum Match 0%	Maximum Match 100%	Listing first 45 summaries
Database : SwissProt_39.*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
Result No.	Score	Query	Length	DB ID	Description
1	295	100.0	618	I BIR3_HUMAN	01490 homo sapien
2	290	98.3	611	I BIR2_CHICK	09660 gallus gallus
3	282	95.6	358	I PIAP_PIG	06240 sus scrofa
4	282	95.6	604	I BIR2_HUMAN	01489 homo sapien
5	282	95.6	612	I BIR3_MOUSE	06210 mus musculus
6	268	90.8	600	I IAP3_NEVOP	00866 mus musculus
7	198	26.8	1	I IAP2_NEVOP	P41437 org11a Pseu
8	187	63.4	1403	I BIR2_MOUSE	09136 mus musculus
9	186	63.1	1402	I BIR2_MOUSE	09133 mus musculus
10	186	63.1	1403	I BIR2_MOUSE	09135 mus musculus
11	186	63.1	1403	I BIR2_MOUSE	09116 mus musculus
12	183	62.0	1447	I BIR2_MOUSE	09494 mus musculus
13	182	61.7	275	I TNF_GYCP	P4136 cydia pomonella
14	178	60.3	1403	I BIR2_HUMAN	013059 homo sapien
15	174	59.9	1	I BIR4_MOUSE	060589 mus musculus
16	174	59.9	495	I BIR4_MOUSE	09116 rattus norvegicus
17	174	59.9	497	I BIR4_HUMAN	09117 homo sapien
18	160	54.2	438	I BIR2_DROME	024306 drosophila
19	156	52.9	498	I IAP2_DIHOX	P42307 dirosophila
20	118	20.0	286	I IAP1_NEVAC	P41435 autographa
21	117.5	39.8	4829	I BIR2_HUMAN	090919 homo sapien
22	111	37.6	1	I IAP1_NEVOP	010296 org11a Pseu
23	110	37.3	239	I ZFP1_IRF6	P41732 chilo lindae
24	104	35.3	997	I BIR2_SEPHO	014664 schizosaccharomyces pombe
25	90.5	30.7	140	I BIR5_MOUSE	070301 mus musculus
26	90.5	30.7	142	I BIR5_RAT	097917 rattus norvegicus
27	87.5	29.7	142	I BIR5_HUMAN	015392 homo sapien
28	67.5	22.9	224	I IAP1_ASFB7	065338 african swi
29	65.5	22.2	224	I IAP1_ASFB1	014522 african swi
30	61.5	20.8	224	I IAP1_ASFB3	014511 african swi
31	61.5	20.8	224	I IAP1_ASFB	012407 african swi
32	61.5	20.8	238	I IAP1_XENLA	011533 african swi
33	58.5	17.8	1173	I TSPL_XENLA	P35448 xenopus lae

RESULT	1	BIR3_HUMAN	ID	BIR3_HUMAN	STANDARD:	PRT;	618 AA.
RN	[2]	SEQUENCE FROM N.A.	RC	TISSUE=Liver;	RC		
RN		SEQUENCE FROM N.A.	RC	MEDLINE=914949; Pubmed=8552191;	RA		
RN		TISSUE=Liver;	RC	liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cheerton-Horvat G., Parahian R., McLean T., Ikeda J., Mackenzie A., Korneluk R. G.; "Suppression of apoptosis in mammalian cells by IAP and a related family of IAP genes"; Nature 379:349-353(1996).	RA		
RN		SEQUENCE FROM N.A.	RC	"[3]"	RA		
RN		TISSUE=Fetal liver;	RC	"[4]"	RA		
RN		STRUCTURE BY NMR OF 266-263.	RR	STRUCTURE BY NMR OF 266-263.	RA		
RN		MEDLINE=9020943; PubMed=8643514;	RR	MEDLINE=9020943; PubMed=8643514;	RA		
RN		P4136 cydia pomonella	RR	P4136 cydia pomonella	RA		
RN		P41435 autographa	RR	P41435 autographa	RA		
RN		090919 homo sapien	RR	090919 homo sapien	RA		
RN		010296 org11a Pseu	RR	010296 org11a Pseu	RA		
RN		P41732 chilo lindae	RR	P41732 chilo lindae	RA		
RN		014664 schizosaccharomyces pombe	RR	014664 schizosaccharomyces pombe	RA		
RN		070301 mus musculus	RR	070301 mus musculus	RA		
RN		097917 rattus norvegicus	RR	097917 rattus norvegicus	RA		
RN		015392 homo sapien	RR	015392 homo sapien	RA		
RN		P35448 xenopus lae	RR	P35448 xenopus lae	RA		
RN		P16554_drosophila	CC	P16554_drosophila	CC		
RN		P36659_homo_sapien	CC	P36659_homo_sapien	CC		
RN		Q05355_streptomyces	CC	Q05355_streptomyces	CC		
RN		Q03277_scilla_copae	CC	Q03277_scilla_copae	CC		
RN		Q27287_saccharomyces	CC	Q27287_saccharomyces	CC		
RN		P22579_saccharomyces	CC	P22579_saccharomyces	CC		
RN		Q02973_arabidopsis	CC	Q02973_arabidopsis	CC		
RN		P41454_saccharomyces	CC	P41454_saccharomyces	CC		
RN		P18856_ephydita_m	CC	P18856_ephydita_m	CC		
RN		Q28178_bos_tauris	CC	Q28178_bos_tauris	CC		
RN		P07996_homo_sapien	CC	P07996_homo_sapien	CC		

CC -!- SIMILARITY: BELONGS TO THE IAP FAMILY.  
 CC -!- SIMILARITY: CONTAINS 3 BIR REPEATS.  
 CC -!- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

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DR EMBL: LA9431; AC:AC1942; 1;  
 DR EMBL: US5879; AC:AC50372; 1;  
 DR EMBL: US5547; AC:AC5508; 1; -  
 DR PDB: 1QBR; 20-OCT-99.  
 DR MIM: 601721; -  
 DR InterPro: IPRO01170; BIR.  
 DR InterPro: IPRO01315; CARD.  
 DR InterPro: IPRO01341; Znf\_fing.  
 DR Pfam: PF00653; BIR; 3;  
 DR Pfam: PF00619; CARD; 1;  
 DR SMART: SM00238; BIR; 3;  
 DR SMART: SM00114; CARD; 1;  
 DR SMART: SM0014; RING; 1;  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 3;  
 DR PROSITE: PS0143; BIR\_REPEAT\_2; 3;  
 DR PROSITE: PS50209; CARD; 1;  
 KW Apoptosis; Zinc-finger; Repeat; 3D-structure.  
 FT REPEAT 46 113 BIR 1.  
 FT REPEAT 184 250 BIR 2.  
 FT REPEAT 269 336 BIR 3.  
 FT DOMAIN 453 539 CARD.  
 FT 2N\_FING 571 605 RING-TYPE.  
 FT CONFLICT 308 308 S->P (IN REF. 2).  
 FT CONFLICT 414 414 C->G (IN REF. 2).  
 FT CONFLICT 514 514 Q->W (IN REF. 2).  
 FT SEQUENCE 618 AA: 69899 MW: C1778D328063586D CRC64:

Query Match 100 %; Score 295; DB 1; Length 618;  
 Best Local Similarity 100 %; Pred. No. 4.4e-29; Gaps 0;  
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PEQLASAGFVYGRNDVKCFCGGLRCWESGDPWNEHAKWPRCE 48  
 DB 287 PEQLASAGFVYGRNDVKCFCGGLRCWESGDDFWNEHAKWPRCE 334

RESULT 2  
 BIR\_CLICK STANDARD: PRT: 611 AA.  
 ID BIR\_CHICK  
 AC 090600;  
 DT 01-NOV-1997 (Rel. 35, created)  
 DT 20-AUG-2001 (Rel. 40, last annotation update)  
 DE INHIBITOR OF APOPTOSIS PROTEIN (IAP) (INHIBITOR OF T CELL APOPTOSIS PROTEIN).  
 GN ITPA.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
 OC Gallus.  
 RN 11) NCBI\_TAXID=9031;  
 RP SEQUENCE FROM N A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=98162622; PubMed=9501011;  
 RX MEDLINE=9710112; PubMed=8945639;  
 RX DIGBY M.R., Kimpson W.G., York J.J., Connick T.B., Lowenthal J.W.; RT \*ITA, a vertebrate homologue of IAP that is expressed in T

CC -!- SIMILARITY: BELONGS TO THE IAP FAMILY.  
 CC -!- SIMILARITY: CONTAINS 3 BIR REPEATS.  
 CC -!- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

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DR EMBL: U27466; AAB8118; 1; -  
 DR InterPro: IPRO01315; CARD.  
 DR InterPro: IPRO01841; Znf\_fing.  
 DR Pfam: PF00653; BIR; 3;  
 DR Pfam: PF00619; CARD; 1;  
 DR SMART: SM00238; BIR; 3;  
 DR SMART: SM00114; CARD; 1;  
 DR SMART: SM0018; RING; 1;  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 3;  
 DR PROSITE: PS0143; BIR\_REPEAT\_2; 3;  
 DR SMART: SM00238; BIR; 3;  
 DR SMART: SM00114; CARD; 1;  
 DR SMART: SM0018; RING; 1;  
 DR PROSITE: PS50209; CARD; 1;  
 KW Apoptosis; Zinc-finger; Repeat; Nuclear protein.  
 FT REPEAT 176 242 BIR 1.  
 FT REPEAT 262 329 BIR 3.  
 FT ZN\_FING 564 598 RING-TYPE.  
 FT SEQUENCE 611 AA: 69009 MW: 53PC9136F34EBDD CRC64:

Query Match 98.3%; Score 290; DB 1; Length 611;  
 Best Local Similarity 95.8%; Pred. No. 1.8e-28; Gaps 0;  
 Matches 45; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 PEQLASAGFVYGRNDVKCFCGGLRCWESGDPWNEHAKWPRCE 48  
 DB 280 PEQLADAGFVYGRNDVKCFCGGLRCWESGDDFWNEHAKWPRCE 327

RESULT 3  
 PIP\_PIG STANDARD: PRT: 358 AA.  
 ID PIP\_PIG  
 AC 062640;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, last annotation update)  
 DE POTENTIVE INHIBITOR OF APOPTOSIS.  
 GN PIAP.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Sulina; Sulidae; Sus.  
 OC Mammalia; Eutheria; Cetartiodactyla; Sulina; Sulidae; Sus.  
 OX NCBI\_TAXID=9823;  
 RN 1) SEQUENCE FROM N A.  
 RP TISSUE=Aorta;  
 RX MEDLINE=98162622; PubMed=9501011;  
 RX Stehlík C, de Martino R, Binder B.R., Lipp J;  
 RX "Cytokine induced expression of Porcine Inhibitor of apoptosis protein (PIAP) family member is regulated by NF-kappa B.";  
 RT Biophys. Res. Commun. 243:827-832(1998).  
 RC -!- SIMILARITY: BELONGS TO THE IAP FAMILY.



RESULT 5							
BIR3_MOUSE	95.6%	Score 282; DB 1;	length 604;	KW	Apoptosis; zinc-finger; Repeat.		
ID	BIR3_MOUSE	STANDARD;	PRT;	FT	REPEAT	46	113
AC	06220;	008864;		FT	REPEAT	177	243
DT	01-Nov-1997	(Rel. 35, Created)		FT	REPEAT	262	329
DY	01-Nov-1997	(Rel. 35, last sequence update)		FT	DOMAIN	447	533
DT	20-AUG-2001	(Rel. 40, last annotation update)		FT	ZN FING	565	599
DE	BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (MIAP2) (MIAP-2).			FT	CONFLICT	380	380
GN	BIRC3 OR API2 OR IAP2.			FT	SEQUENCE	612 AA;	69676 MW;
OS	MUS musculus (Mouse);			RA	PEOLASAGFYYVDRNDVKCFCDDGGLRCWESGDPWTHAKWFPRCE 320		E08969D93C6C6100 CRC64;
OC	Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.						
OX	NCBI_TAXID=10090;						
RN	[1]						
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.						
RX	MEDLINE=96128127; Pubmed=8548810;						
RA	Nothe M., Pan M.-G., Renzel W.J., Ayres T.M., Goeddel D.V.;						
RT	"The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.";						
RL	Cell 83:1243-1252(1995).						
RN	[2]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE-Skeletal muscle;						
RX	MEDLINE=98110590; Pubmed=9441758;						
RA	Liston P., Fong W.G., Xuan J.Y., Korneluk R.G.;						
RT	"Genomic characterization of the mouse inhibitor of apoptosis protein 1 and 2 genes";						
CC	-I- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAFL AND TRAF2) TO FORM AN HETEROERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).						
CC	-I- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).						
CC	-I- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SPLEEN, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY, AND TESTIS.						
CC	-I- SIMILARITY: BELONGS TO THE IAP FAMILY.						
CC	-I- SIMILARITY: CONTAINS 3 BIR REPEATS.						
CC	-I- SIMILARITY: CONTAINS 1 CARD DOMAIN.						
CC	-I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.						
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CC	[...]						
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CC	[...]						
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CC	[...]						
CC	EMBL: L49433; AAC42078; 1.;						
DR	EMBL: U88909; AAC53521; 1.;						
DR	MGI: 1197007; Birc3.						
DR	InterPro: IPR001370; BIR.						
DR	InterPro: IPR001315; CARD.						
DR	InterPro: IPR001841; Znf_fing.						
DR	Pfam: PF00653; BIR; 3.						
DR	Pfam: PF00619; CARD; 1.						
DR	Pfam: PF00097; f_C3HC4; 1.						
DR	SMART: SM00238; BIR; 3.						
DR	SMART: SM00114; CARD; 1.						
DR	SMART: SM00184; RING; 1.						
DR	PROSITE: PS01282; BIR_REPEAT_1; 3.						
DR	PROSITE: PS01283; BIR_REPEAT_2; 3.						
DR	PROSITE: PS50209; CARD; 1.						

SO	SEQUENCE	268 AA;	30076 MW;	DF8915FDEB5A/08 CRC64;
QY	1	PEQIASAGCYYVGRNDVKFCGCGGLRCWESGDDPWRERAKWPRCE 48		
Query Match	67.1%	Score 198; DB 1;	Length 268;	
Best Local Similarity	60.4%	Pred. No. 1 ge-1;		
Matches	29;	Conservative	8;	Mismatches 11; Indels 0; Gaps 0;
kw	APOPTOSIS; zinc-finger; Repeat.			
pt	BIR 1.			
pt	REPEAT 27 94			
pt	REFBT 157 233	BIR 2.		
pt	REPEAT 253 320	BIR 3.		
pt	REPEAT 44 512	CARD		
pt	DOMAIN 553 587	RING-TYPE		
ft	ZN_FINGER 500 AA;	AD7F73E8A9317D1 CRC64;		
sq	SEQUENCE 67198 MW;			
db	2 EOLASAFYGFYVGHSDVKFCGCGGLRCWESGDDPWRERAKWPRCE 318			
QY	2	PEQLASAGCYYVGRNDVKFCGCGGLRCWESGDDPWRERAKWPRCE 48		
Query Match	90.8%	Score 268; DB 1;	Length 600;	
Best Local Similarity	89.4%	Pred. No. 9. 2e-26;		
Matches	42;	Conservative	3;	Mismatches 2; Indels 0; Gaps 0;
kw	APOPTOSIS; zinc-finger; Repeat.			
pt	BIR 1.			
pt	REPEAT 7			
pt	IAP3_NPYOP STANDARD; PRT; 268 AA.			
pt	ID IAP3_NPYOP STANDARD; PRT; 268 AA.			
ac	P41437;			
dt	01-NOV-1995 (Rel. 32, Created)			
dt	01-NOV-1995 (Rel. 32, Last sequence update)			
dt	20-AUG-2001 (Rel. 40, Last annotation update)			
de	APOPTOSIS INHIBITOR 3 (IAP-3).			
gn	IAP3 OR IAP			
os	Oryzias pseudotsgata multicapsid polyhedrosis virus (OpMNPyV).			
oc	Viruses; dsDNA viruses, no RNA stage; Baculoviridae;			
ox	Nucleopolyhedrovirus.			
rn	[1]			
rp	SEQUENCE FROM N.A.			
rx	MEDLINE-#9418709J; PubMed=819034;			
ra	Birnbaum M.J., Clem R.J., Miller L.K.;			
rt	"An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a polypeptide with Cys/His sequence motifs".			
rl	J. Virol. 68:2521-2528(1994).			
rn	[2]			
rp	SEQUENCE FROM N.A.			
rx	MEDLINE-#9271300; PubMed=9126251;			
ra	Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S., Rothmann G.F.			
rt	"The sequence of the Oryzias pseudotsgata multinucleocapsid nuclear polyhedrosis virus genome."			
rl	Virology 229:381-389(1997).			
cc	- - - FUNCTION: ACTS BY BLOCKING CELLULAR APOPTOSIS RATHER THAN BY PREVENTING VIRAL STIMULATION OF APOPTOSIS.			
cc	- - - SIMILARITY: CONTAINS 2 BIR REPEATS.			
cc	- - - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.			
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cc	EMBL: I2Z564; AAC02610-1; PROSITE: PS01282; BIR_REPEAT_1; DR			
cc	EMBL: U75930; AAC59034-1; PROSITE: PS01413; BIR_REPEAT_2; DR			
cc	EMBL: YP00053; BIR_REPEAT_3; DR			
cc	EMBL: YP00053; BIR_REPEAT_4; DR			
cc	EMBL: YP00053; BIR_REPEAT_5; DR			
cc	EMBL: YP00053; BIR_REPEAT_6; DR			
cc	EMBL: YP00053; BIR_REPEAT_7; DR			
cc	EMBL: YP00053; BIR_REPEAT_8; DR			
cc	EMBL: YP00053; BIR_REPEAT_9; DR			
cc	EMBL: YP00053; BIR_REPEAT_10; DR			
cc	EMBL: YP00053; BIR_REPEAT_11; DR			
cc	EMBL: YP00053; BIR_REPEAT_12; DR			
cc	EMBL: YP00053; BIR_REPEAT_13; DR			
cc	EMBL: YP00053; BIR_REPEAT_14; DR			
cc	EMBL: YP00053; BIR_REPEAT_15; DR			
cc	EMBL: YP00053; BIR_REPEAT_16; DR			
cc	EMBL: YP00053; BIR_REPEAT_17; DR			
cc	EMBL: YP00053; BIR_REPEAT_18; DR			
cc	EMBL: YP00053; BIR_REPEAT_19; DR			
cc	EMBL: YP00053; BIR_REPEAT_20; DR			
cc	EMBL: YP00053; BIR_REPEAT_21; DR			
cc	EMBL: YP00053; BIR_REPEAT_22; DR			
cc	EMBL: YP00053; BIR_REPEAT_23; DR			
cc	EMBL: YP00053; BIR_REPEAT_24; DR			
cc	EMBL: YP00053; BIR_REPEAT_25; DR			
cc	EMBL: YP00053; BIR_REPEAT_26; DR			
cc	EMBL: YP00053; BIR_REPEAT_27; DR			
cc	EMBL: YP00053; BIR_REPEAT_28; DR			
cc	EMBL: YP00053; BIR_REPEAT_29; DR			
cc	EMBL: YP00053; BIR_REPEAT_30; DR			
cc	EMBL: YP00053; BIR_REPEAT_31; DR			
cc	EMBL: YP00053; BIR_REPEAT_32; DR			
cc	EMBL: YP00053; BIR_REPEAT_33; DR			
cc	EMBL: YP00053; BIR_REPEAT_34; DR			
cc	EMBL: YP00053; BIR_REPEAT_35; DR			
cc	EMBL: YP00053; BIR_REPEAT_36; DR			
cc	EMBL: YP00053; BIR_REPEAT_37; DR			
cc	EMBL: YP00053; BIR_REPEAT_38; DR			
cc	EMBL: YP00053; BIR_REPEAT_39; DR			
cc	EMBL: YP00053; BIR_REPEAT_40; DR			
cc	EMBL: YP00053; BIR_REPEAT_41; DR			
cc	EMBL: YP00053; BIR_REPEAT_42; DR			
cc	EMBL: YP00053; BIR_REPEAT_43; DR			
cc	EMBL: YP00053; BIR_REPEAT_44; DR			
cc	EMBL: YP00053; BIR_REPEAT_45; DR			
cc	EMBL: YP00053; BIR_REPEAT_46; DR			
cc	EMBL: YP00053; BIR_REPEAT_47; DR			
cc	EMBL: YP00053; BIR_REPEAT_48; DR			
cc	EMBL: YP00053; BIR_REPEAT_49; DR			
cc	EMBL: YP00053; BIR_REPEAT_50; DR			
cc	EMBL: YP00053; BIR_REPEAT_51; DR			
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cc	EMBL: YP00053; BIR_REPEAT_82; DR			
cc	EMBL: YP00053; BIR_REPEAT_83; DR			
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cc	EMBL: YP00053; BIR_REPEAT_204; DR			
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cc	EMBL: YP00053; BIR_REPEAT_212; DR		</td	

Query Match 63.1%; Score 185; DB 1; Length 1402;  
 Best Local Similarity 60.4%; Pred. No. 2.6e-15; Mismatches 6; Indels 0; Gaps 0;

RESULT 10  
 BIRG\_MOUSE STANDARD PRT: 1403 AA.

BIRG\_MOUSE STANDARD PRT: 1402 AA.

AC Q9W43; Q9R07; Q9JBS;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DE BACULOVIRAL REP-CONTAINING PROTEIN 1A (NEURONAL APOPTOSIS INHIBITORY PROTEIN 1).  
 DE BIRC OR NAIP.  
 OS MUS musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Endrizzi M.G., Hadinoto V., Groomey J.D., Miller W., Dietrich W.F.;  
 RT "Genomic sequence analysis of the mouse Naip gene array.";  
 RL Genome Res. 10:105-110(2000).  
 CC -!- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF SIGNALS.  
 CC -!- SIMILARITY: CONTAINS 3 BIR REPEATS.  
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 CC EMBL: AF24243; AFM8249\_1; -.  
 DR EMBL; MGII:185856; Bircg.  
 DR Interpro: IPR01370; BIR.  
 DR Pfam: PF0053; BIR; 3.  
 DR SMART: SM0023; BIR; 3.  
 DR PROSITE: PS0128; BIR\_REPEAT\_1; 2.  
 DR PROSITE: PS5043; BIR\_REPEAT\_2; 3.  
 KW Apoptosis; Repeat; Multigene family.  
 KW Apoptosis; Repeat; Multigene family.  
 FT REPEAT 60 127 BIR 1.  
 FT REPEAT 159 227 BIR 2.  
 FT REPEAT 278 345 BIR 3.  
 FT REPEAT 343 343 I -> V (IN REF. 2).  
 FT REPEAT 359 359 L -> Q (IN REF. 2).  
 FT CONFLICT 624 624 E -> K (IN REF. 2).  
 FT CONFLICT 1092 1092 D -> E (IN REF. 3).  
 FT CONFLICT 1116 1116 D -> N (IN REF. 3).  
 FT CONFLICT 1123 1123 G -> R (IN REF. 3).  
 FT CONFLICT 1129 1129 L -> H (IN REF. 1).  
 FT CONFLICT 1140 1140 T -> M (IN REF. 2).  
 FT CONFLICT 1269 1269 A -> V (IN REF. 3).  
 SQ SEQUENCE 1402 AA: CIDFFBA359893E0D CRC64;  
 SQ 1 PEQLASAGFVYVRNDPKCFCGCGLRWEQEGDPWAEHKWFPRCE 48  
 Db 178 PRVLSAAGFVFTKRDIVOCSCCGSIGNNEGDDPWEHKWFPRCE 225  
 Query Match 63.1%; Score 186; DB 1; Length 1403;  
 Best Local Similarity 60.4%; Pred. No. 2.6e-15; Mismatches 6; Indels 0; Gaps 0;

RESULT 11  
 BIRG\_MOUSE STANDARD PRT: 1403 AA.

AC Q9R016; Q9R029; P81703; Q9122; Q9121;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DE BACULOVIRAL REP-CONTAINING PROTEIN 1A (NEURONAL APOPTOSIS INHIBITORY PROTEIN 1).  
 DE BIRC OR NAIP.  
 OS MUS musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TAXID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yaraghi Z., Korneljuk R.G., Mackenzie A.E.;  
 RT "Cloning and characterization of the multiple copies of the murine homologue of Naip (neuronal apoptosis inhibitory protein)." ; Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:99A31676; PubMed:10501978;  
 RA Huang S., Scharff J.M., Groomey J.D., Endrizzi M.G., Dietrich W.F.;  
 RT "The mouse Naip gene cluster on Chromosome 13 encodes several distinct functional transcripts." ;  
 RL Mamm. Genome 10:1032-1035(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:20414747; PubMed:10958627;  
 RA Endrizzi M.G., Hadinoto V., Groomey J.D., Miller W., Dietrich W.F.;  
 RT Genomic sequence analysis of the mouse Naip gene array. ;  
 RL Genome Res. 10:1095-1102(2000).  
 CC -!- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF SIGNALS.  
 CC -!- SIMILARITY: CONTAINS 3 BIR REPEATS.  
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 CC EMBL: AF007769; AAB69223; 1.  
 DR EMBL: AF135491; AD56763; 1.  
 DR EMBL: AF22432; AAB8752; 1.  
 DR MGD: MGI:1288223; Bircia.  
 DR Interpro: IPR01370; BIR.  
 DR Pfam: PF0053; BIR; 3.  
 DR SMART: SM00238; BIR; 3.  
 DR PROSITE: PS0128; BIR\_REPEAT\_1; 1.  
 DR PROSITE: PS50133; BIR\_REPEAT\_2; 3.  
 KW Apoptosis; Repeat; Multigene family.  
 FT REPEAT 159 227 BIR 2.  
 FT REPEAT 278 345 BIR 3.  
 FT CONFLICT 343 343 I -> V (IN REF. 2).  
 FT CONFLICT 359 359 L -> Q (IN REF. 2).  
 FT CONFLICT 624 624 E -> K (IN REF. 2).  
 FT CONFLICT 1092 1092 D -> E (IN REF. 3).  
 FT CONFLICT 1116 1116 D -> N (IN REF. 3).  
 FT CONFLICT 1123 1123 G -> R (IN REF. 3).  
 FT CONFLICT 1129 1129 L -> H (IN REF. 1).  
 FT CONFLICT 1140 1140 T -> M (IN REF. 2).  
 FT CONFLICT 1269 1269 A -> V (IN REF. 3).  
 SQ SEQUENCE 1403 AA: B31630259595EE67 CRC64;  
 SQ 1 PEQLASAGFVYVRNDPKCFCGCGLRWEQEGDPWAEHKWFPRCE 48  
 Db 178 PRVLSAAGFVFTKRDIVOCSCCGSIGNNEGDDPWEHKWFPRCE 225  
 Query Match 63.1%; Score 186; DB 1; Length 1403;  
 Best Local Similarity 60.4%; Pred. No. 2.6e-15; Mismatches 6; Indels 0; Gaps 0;

DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 1E (NEURONAL APOPTOSIS  
DE INHIBITORY PROTEIN 5).  
GN BIRCLE OR NAIP OR NAIP-RS3.  
OS MUS musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NEBL\_TaxID=10090;  
RN [1].  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9943166; PubMed=10501978;  
RA Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.;  
RT "The mouse Naip gene cluster on Chromosome 13 encodes several distinct  
functional transcripts."  
RL Mamm. Genome 10:1032-1035(1999).  
RN [2].  
RP SEQUENCE FROM N.A.  
RX SPRAIN=129/SV:  
RA MEDLINE=97131520; PubMed=8975718;  
RA Schaff J.M., Damon D., Frisella A., Bruno S., Beggs A.H.,  
RK Kunkel L.M., Miller W., Dietrich W.F.;  
RT "Comparative sequence analysis of the mouse and human Lgln1/SMA  
interval".  
RL Genomics 60:137-151(1999).  
RN [3].  
RP SEQUENCE OF 82-168 FROM N.A.  
RC SPRAIN=129/SV:  
RA MEDLINE=97131520; PubMed=8975718;  
RA Schaff J.M., Damon D., Frisella A., Bruno S., Beggs A.H.,  
RK Kunkel L.M., Miller W., Dietrich W.F.;  
RT "The mouse region syntentic for human spinal muscular atrophy lies  
within the Lgln1 critical interval and contains multiple copies of Naip  
exon 5."  
RL Genomics 38:405-417(1995).  
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF  
CC SIGNALS.  
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC  
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or send an email to license@isb-sib.ch).  
CC  
DR EMBL: AF135492; AND556764; 1; .  
DR EMBL: AF135492; AND556764; 1; .  
DR EMBL: U66136; AAC52974; 1; .  
DR MGDB: MGI:1298220; BIR.  
DR InterPro: IPR001370; BIR.  
DR Pfam: PF0053; BIR; 3.  
DR SMART: SM00238; BIR; 3.  
DR PROSITE: PS01262; BIR\_REPEAT\_1; 2.  
DR PROSITE: PS5013; BIR\_REPEAT\_2; 3.  
KW Apoptosis; Repeat: Multigene family.  
FT REPEAT: 60 127 BIR 1.  
FT REPEAT: 159 227 BIR 2.  
FT REPEAT: 278 345 BIR 3.  
FT COMFLICT: 92 92 K -> R (IN REF. 1).  
FT COMFLICT: 144 144 S -> R (IN REF. 1).  
FT COMFLICT: 242 242 S -> G (IN REF. 2).  
FT COMFLICT: 472 472 T -> A (IN REF. 2).  
FT COMFLICT: 516 516 A -> D (IN REF. 2).  
FT COMFLICT: 521 521 A -> T (IN REF. 2).  
FT COMFLICT: 533 533 V -> A (IN REF. 2).  
FT COMFLICT: 538 538 S -> I (IN REF. 2).  
FT COMFLICT: 1092 1092 E -> D (IN REF. 2).  
FT COMFLICT: 1129 1129 H -> L (IN REF. 2).  
FT COMFLICT: 1137 1137 R -> Q (IN REF. 2).  
FT COMFLICT: 1242 1242 V -> I (IN REF. 2).  
FT COMFLICT: 1276 1276 D -> N (IN REF. 2).  
SQ SEQUENCE AA; 159695 MW; B27F645043BCCE42 CRC64;

DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 1B (NEURONAL APOPTOSIS  
DE INHIBITORY PROTEIN 2).  
GN BIRCB OR NAIP2 OR NAIP-RS6.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NEBL\_TaxID=10090;  
RN [1].  
RP SEQUENCE FROM N.A.  
RX SPRAIN=129/SV:  
RA MEDLINE=9943166; PubMed=10501978;  
RA Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.;  
RT "The mouse Naip gene cluster on Chromosome 13 encodes several distinct  
functional transcripts."  
RL Mamm. Genome 10:1032-1035(1999).  
RN [2].  
RP SEQUENCE OF 82-168 FROM N.A.  
RX SPRAIN=129/SV:  
RA MEDLINE=9943166; PubMed=10501978;  
RA Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.;  
RT "The mouse Naip gene cluster on Chromosome 13 encodes several distinct  
functional transcripts."  
RL Mamm. Genome 10:1032-1035(1999).  
RN [3].  
RP SEQUENCE OF 82-168 FROM N.A.  
RX SPRAIN=129/SV:  
RA MEDLINE=9943166; PubMed=10501978;  
RA Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.;  
RT "The mouse Naip gene cluster on Chromosome 13 encodes several distinct  
functional transcripts."  
RL Mamm. Genome 10:1032-1035(1999).  
RN [4].  
RP SEQUENCE OF 82-168 FROM N.A.  
RX SPRAIN=129/SV:  
RA MEDLINE=97131520; PubMed=8975718;  
RA Schaff J.M., Damon D., Frisella A., Bruno S., Beggs A.H.,  
RK Kunkel L.M., Miller W., Dietrich W.F.;  
RT "The mouse region syntentic for human spinal muscular atrophy lies  
within the Lgln1 critical interval and contains multiple copies of Naip  
exon 5."  
RL Genomics 38:405-417(1995).  
RN [5].  
RP SEQUENCE OF 82-168 FROM N.A.  
RX SPRAIN=129/SV:  
RA MEDLINE=97131520; PubMed=8975718;  
RA Schaff J.M., Damon D., Frisella A., Bruno S., Beggs A.H.,  
RK Kunkel L.M., Miller W., Dietrich W.F.;  
RT "The mouse region syntentic for human spinal muscular atrophy lies  
within the Lgln1 critical interval and contains multiple copies of Naip  
exon 5."  
RL Genomics 38:405-417(1995).  
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF  
CC SIGNALS.  
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC  
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CC  
DR EMBL: AF135492; AND556761; 1; .  
DR EMBL: AF135492; AND56021; 1; .  
DR EMBL: AF135492; AND56759; 1; .  
EMBL: AF131205; AND556760; 1; .

DR EMBL; U66329; AAC52977.1; -.  
 DR MGD; MGI:1298226; Birdb.  
 DR InterPro; IPR01370; BIR.  
 DR Pfam; PF00653; BIR; 3.  
 DR SMART; SM00238; BIR; 3.  
 DR PROSITE; PS01242; BIR\_REPEAT\_1; 2.  
 DR PROSITE; PS01433; BIR\_REPEAT\_2; 3.  
 KW Apoptosis; Repeat; Multigene family.  
 FT REPEAT 60 127 BIR 1.  
 FT REPEAT 150 227 BIR 2.  
 FT REPEAT 278 345 BIR 3.  
 FT CONFLICT 377 377 D -> G ((IN REF. 3)).  
 FT CONFLICT 403 403 L -> F ((IN REF. 3)).  
 FT CONFLICT 478 478 L -> I ((IN REF. 3)).  
 FT CONFLICT 540 540 N -> Y ((IN REF. 3)).  
 FT CONFLICT 862 862 K -> N ((IN REF. 3)).  
 FT CONFLICT 1079 1080 SD -> P ((IN REF. 3)).  
 FT CONFLICT 1089 1115 R -> C ((IN REF. 3)).  
 FT CONFLICT 1115 1115 K -> E ((IN REF. 3)).  
 FT CONFLICT 1122 1122 T -> A ((IN REF. 3)).  
 FT CONFLICT 1136 1136 D -> E ((IN REF. 3)).  
 FT CONFLICT 1157 1157 S -> G ((IN REF. 3)).  
 FT CONFLICT 1271 1271 F -> C ((IN REF. 3)).  
 SO SEQUENCE 1447 AA; 164033 MW; 9BFG6A73BAE602 CRC64;

Query Match 62.0%; Score 183; DB 1; Length 1447;  
 Best Local Similarity 60.4%; Pred. No. 6.4e-15; Matches 29; Conservative 6; Mismatches 13; Indels 0; Gaps 0; OQ 1 PEOLASAGFYVGRNDDVKCFCGGLRWESEGDPWAEHAKWFRC 48  
 AC | : ||| : | : | : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : 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 CC EMBL; LO5494; ARRA3353.1; -.  
 DR SMART; U53466; ARB3998.1; -.  
 DR InterPro; IPR01370; BIR.  
 DR PROSITE; PS01841; Znf\_fing.  
 DR SMART; SM00238; BIR; 2.  
 DR PROSITE; PS01281; BIR\_REPEAT\_1; 2.  
 DR PROSITE; PS01414; BIR\_REPEAT\_2; 2.  
 KW Apoptosis; Zinc-finger; Repeat.  
 FT REPEAT 7 73 BIR 1.  
 FT REPEAT 108 175 BIR 2.  
 FT ZNFING 226 RING-TYPE.  
 SQ SEQUENCE 275 AA; 31290 MW; 8460544869CAAD60 CRC64;  
 DR 126 PEGMADAGFFTYGIGDNKCFICGGGLKDWPEDVPWEOHVRMEFRC 172  
 DR  
 Query Match 61.7%; Score 182; DB 1; Length 275;  
 Best Local Similarity 59.6%; Pred. No. 1.8e-15; Matches 28; Conservative 6; Mismatches 13; Indels 0; Gaps 0;  
 OQ 1 PEOLASAGFYVGRNDDVKCFCGGLRWESEGDPWAEHAKWFRC 47  
 AC Q13015; Q13730; Q99196; O75857;  
 DT 01-NOV-1997 (Ref. 35; Created)  
 DT 20-AUG-2001 (Ref. 40; Last sequence update)  
 DT 20-AUG-2001 (Ref. 40; Last annotation update)  
 DE BACULOVIRAL IP\_REPEAT-CONTAINING PROTEIN 1 (NEURONAL APOPTOSIS INHIBITOR PROTEIN).  
 GN BIR1 OR NAIP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1] NCBI\_TAXID=9606;  
 RP SEQUENCE FROM N.A..  
 RC TISSUE=Fetal brain;  
 RX MEDLINE-B95112344; Pubmed=7813013;  
 RA Roy N., Mandelov M.S., McLean M., Shuttler G., Yaraghi Z.,  
 RA Farhadi R., Baird S., Besner-Johnston A., Defeuvre C., Kang X.,  
 RA Salim M., Aubry J., Tamai K., Guan X., Ioannou P., Crawford T.O.,  
 RA de Jong P.J., Surh L., Ikeda J., Korneluk R.G., Mackenzie A.;  
 RA "The gene for neuronal apoptosis inhibitor protein is partially deleted in individuals with spinal muscular atrophy.";  
 RA Cell 80:167-178(1995).  
 RP SEQUENCE FROM N.A., AND REVISIONS.  
 RC TISSUE=Brain;  
 RX MEDLINE-B98163755; Pubmed=9803025;  
 RA Chen Q., Baird S.D., Besner-Johnston A., Farhadi R.,  
 RA Mackenzie A.E.;  
 RA "Sequence of a 131-kb region of S913.1, containing the spinal muscular atrophy candidate genes SMN and NAIP.",  
 RA Genomics 48:121-127(1998).  
 RN [3]  
 RP SEQUENCE OF 386-623 FROM N.A.  
 RA Xuan J.-Y., Kang X., Lerebvre C., Ikeda J.-E., Korneluk R.,  
 RA Annavino R., Velona L., Brabe C., Scheffler H., van Ommen G.J.B.,  
 RA Buis C.H.C.M.;  
 RA Submitted (MAY-1995) to the EMBL/GenBank/DDJB databases.  
 RN [4]  
 RP SEQUENCE OF 222-1403 FROM N.A.  
 RA Jones K., Graves T., McPherson J.;  
 RA Submitted (JUN-1996) to the EMBL/GenBank/DDJB databases.  
 RN [5]

BTRC4 OR API3 OR XIFAP OR ALPA OR MIHA..  
 OS MUS musculus (Mouse);  
 OS Marmoseta; Metacercaria; Craniata; Vertebrata; Euteleostomi;  
 OS Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.  
 NCBI\_TAXID=10090;  
 [1] SEQUENCE FROM N.A.  
 RN RP STRAIN=NC57BL/6 X\_CIA; TISSUE=Liver;  
 RX MEDLINE=96209843; PubMed=8143514;  
 RA Uren A.G.; Pakrasi M.; Hawkins C.J.; Puls K.L.; Vaux D.L.;  
 RT \*Cloning and expression of apoptosis inhibitory protein homologs that  
 RT function to inhibit apoptosis and/or bind tumor necrosis factor  
 RT receptor-associated factors\*;  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).  
 [2] SEQUENCE FROM N.A.  
 RA Farahani R.; Lefebvre C.; Korneluk R.G.; Mackenzie A.E.;  
 RA Subramani M.; JUN-1997; to the EMBL/GenBank/DBJ databases.  
 -1- FUNCTION: APOPTIC SUPPRESSOR. INHIBITOR OF CASPASE-3 AND  
 CC CASPASE-7 (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: CYTOSOLIC (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 RING REPEATS.  
 CC ---  
 DR EMBL; U88990; AAB53376.1; --.  
 DR MGI:07572; BIRc4.  
 DR InterPro; IPR001370; BIR.  
 DR InterPro; IPR001841; Znf\_finger.  
 DR Pfam; PF00097; zf-C3HC4\_1.  
 DR SMART; SM00238; BIR\_3.  
 DR SMART; SM00184; RING\_1.  
 DR PROSITE; PS01202; BIR\_REPEAT\_1; 3.  
 DR PROSITE; PS01043; BIR\_REPEAT\_2; 3.  
 KW Apoptosis; Zinc-finger; Repeat.  
 FT REPEAT 26 93 BIR\_1.  
 FT REPEAT 163 230 BIR\_2.  
 FT REPEAT 264 329 BIR\_3.  
 FT ZN\_FING 449 483 RING\_TYPE.  
 FT CONFLICT 208 208 E -> K (IN REF. 2).  
 FT CONFLICT 317 317 E -> D (IN REF. 2).  
 FT CONFLICT 322 322 W -> C (IN REF. 2).  
 FT CONFLICT 346 346 S -> P (IN REF. 2).  
 FT CONFLICT 360 360 S -> P (IN REF. 2).  
 FT CONFLICT 388 388 I -> L (IN REF. 2).  
 FT CONFLICT 449 449 C -> S (IN REF. 2).  
 FT CONFLICT 462 462 V -> F (IN REF. 2).  
 FT CONFLICT 468 468 V -> A (IN REF. 2).  
 FT CONFLICT 490 490 K -> N (IN REF. 2).  
 SEQUENCE 496 AA; 56079 MW; BC5FB1B079F82C0D8 CRC64;

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Query Match      59.0%; Score 174; DB 1; Length 496;
Best Local Similarity 59.6%; Pred. No. 3.1e 14;
Matches 28; Conservative 6; Mismatches 13; Indels 0;
Qy   2 EDLASAGFYVGRNDYKFCOCGIGLRCWESDDPWEVRAKWFPRCE 48
     ||||| ||| ; | 11111 - 111 | : 111 :1111:1;
Db 281 EQLARAGFYALGEKGDKVKCFHCGGLTDWKPSEDPWEHQAKWYPGCK 327

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Tue Jan 8 08:24:00 2002

us-08-569-749-9.rsp

Job time: 1405 sec